

Figure 1

GATCAAACCTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAATTCCTTA
ATAAAAATACAACCTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTCAATATTATTTCTTCTTGTTTTCTTGCTA
CGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAACTGCTTCTAC
TGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAAAATAAACACAGA
ATATAATAAAATGAGATAATCTAGCTTAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTGGATC

FIG. 2A

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      9      18      27      36      45      54
5'  CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      63      72      81      90      99      108
    ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

      117      126      135      144      153      162
    TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                                M  M  V  D  P  N  G  N  E  S  S

      171      180      189      198      207      216
    GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A  T  Y  F  I  L  I  G  L  P  G  L  E  E  A  Q  F  W

      225      234      243      252      261      270
    TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L  A  F  P  L  C  S  L  Y  L  I  A  V  L  G  N  L  T

      279      288      297      306      315      324
    ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    I  I  Y  I  V  R  T  E  H  S  L  H  E  P  M  Y  I  F

      333      342      351      360      369      378
    CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L  C  M  L  S  G  I  D  I  L  I  S  T  S  S  M  P  K

      387      396      405      414      423      432
    ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M  L  A  I  F  W  F  N  S  T  T  I  Q  F  D  A  C  L

      441      450      459      468      477      486
    CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    L  Q  I  F  A  I  H  S  L  S  G  M  E  S  T  V  L  L

      495      504      513      522      531      540
    GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A  M  A  F  D  R  Y  V  A  I  C  H  P  L  R  H  A  T

      549      558      567      576      585      594
    GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    V  L  T  L  P  R  V  T  K  I  G  V  A  A  V  V  R  G

      603      612      621      630      639      648
    GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A  A  L  M  A  P  L  P  V  F  I  K  Q  L  P  F  C  R

```

FIG. 2B

657	666	675	684	693	702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC					
---	---	---	---	---	---
S N I L S H S Y C L H Q D V M K L A					
711	720	729	738	747	756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC					
---	---	---	---	---	---
C D D I R V N V V Y G L I V I I S A					
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT					
---	---	---	---	---	---
I G L D S L L I S F S Y L L I L K T					
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT					
---	---	---	---	---	---
V L G L T R E A Q A K A F G T C V S					
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG					
---	---	---	---	---	---
H V C A V F I F Y V P F I G L S M V					
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC					
---	---	---	---	---	---
H R F S K R R D S P L P V I L A N I					
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG					
---	---	---	---	---	---
Y L L V P P V L N P I V Y G V K T K					
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG					
---	---	---	---	---	---
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT					
---	---	---	---	---	---
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA					
---	---	---	---	---	---
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT					
---	---	---	---	---	---
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC					
---	---	---	---	---	---
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA					
---	---	---	---	---	---

FIG. 2C

1359	1368	1377	1386	1395	1404
AAC TGC TTC	TAC TGA TGG	TTT ACA GCA	TTC TGA GAT	AAG AAT GGT	ACA TCT AGA
---	---	---	---	---	---
1413	1422	1431	1440	1449	1458
GAA CAT TTG	CCA AAG GCC	TAA GCA CGG	CAA AGG AAA	ATA AAC ACA	GAA TAT AAT
---	---	---	---	---	---
1467	1476	1485	1494	1503	1512
AAA ATG AGA	TAA TCT AGC	TTA AAA CTA	TAA CTT CCT	CTT CAG AAC	TCC CAA CCA
---	---	---	---	---	---
1521	1530	1539	1548	1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT CTT	CAA AAT GAC	TTC TAC AGA	GAA GAA ATA
---	---	---	---	---	---
1575	1584	1593	1602	1611	1620
ATT TTT CCT	CTG GAC ACT	AGC ACT TAA	GGG GAA GAT	TGG AAG TAA	AGC CTT GAA
---	---	---	---	---	---
1629	1638	1647	1656	1665	1674
AAG AGT ACA	TTT ACC TAC	GTT AAT GAA	AGT TGA CAC	ACT GTT CTG	AGA GTT TTC
---	---	---	---	---	---
1683	1692	1701	1710	1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC TAT	TTA ATT TTC	TTA TCA ACC	CTT TAA TTA
---	---	---	---	---	---
1737	1746	1755	1764	1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC ATT	GTA GCC ATG	GGA AAA TTG	ATG TTC AGT
---	---	---	---	---	---
1791	1800	1809	1818	1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT CAT	ACA AGT ATA	AAA ATT AAA	AAA AAA AAA
---	---	---	---	---	---
1845	1854	1863	1872	1881	1890
GAC TTC ATG	CCC AAT CTC	ATA TGA TGT	GGA AGA ACT	GTT AGA GAG	ACC AAC AGG
---	---	---	---	---	---
1899	1908	1917	1926	1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG TCT	TAC ATT TTC	TAG AGG AGG	TAT TTA ATT
---	---	---	---	---	---
1953	1962	1971	1980	1989	1998
TCT TCT CAC	TCA TCC AGT	GTT GTA TTT	AGG AAT TTC	CTG GCA ACA	GAA CTC ATG
---	---	---	---	---	---
2007	2016	2025	2034	2043	2052
GCT TTA ATC	CCA CTA GCT	ATT GCT TAT	TGT CCT GGT	CCA ATT GCC	AAT TAC CTG
---	---	---	---	---	---
2061	2070	2079	2088	2097	2106
TGT CTT GGA	AGA AGT GAT	TTC TAG GTT	CAC CAT TAT	GGA AGA TTC	TTA TTC AGA
---	---	---	---	---	---
2115	2124	2133	2142	2151	2160
AAG TCT GCA	TAG GGC TTA	TAG CAA GTT	ATT TAT TTT	TAA AAG TTC	CAT AGG TGA
---	---	---	---	---	---
2169	2178	2187	2196	2205	2214
TTC TGA TAG	GCA GTG AGG	TTA GGG AGC	CAC CAG TTA	TGA TGG GAA	GTA TGG AAT
---	---	---	---	---	---
2223	2232	2241	2250	2259	2268
GGC AGG TCT	TGA AGA TAA	CAT TGG CCT	TTT GAG TGT	GAC TCG TAG	CTG GAA AGT
---	---	---	---	---	---
2277	2286	2295	2304	2313	2322
GAG GGA ATC	TTC AGG ACC	ATG CTT TAT	TTG GGG CTT	TGT GCA GTA	TGG AAC AGG
---	---	---	---	---	---
2331	2340	2349	2358	2367	2376
GAC TTT GAG	ACC AGG AAA	GCA ATC TGA	CTT AGG CAT	GGG AAT CAG	GCA TTT TTG
---	---	---	---	---	---

FIG. 2D

2385	2394	2403	2412	2421	2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA					
---	---	---	---	---	---
2439	2448	2457	2466	2475	2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT					
---	---	---	---	---	---
2493	2502	2511	2520	2529	2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC					
---	---	---	---	---	---
2547	2556	2565	2574	2583	2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT					
---	---	---	---	---	---
2601	2610	2619	2628	2637	2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT					
---	---	---	---	---	---
2655	2664	2673	2682	2691	2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC					
---	---	---	---	---	---
2709	2718	2727	2736	2745	2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT					
---	---	---	---	---	---
2763	2772	2781	2790	2799	2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT					
---	---	---	---	---	---
2817	2826	2835	2844	2853	2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA					
---	---	---	---	---	---
2871	2880	2889	2898	2907	2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT					
---	---	---	---	---	---
2925	2934	2943	2952	2961	2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG					
---	---	---	---	---	---
2979	2988	2997	3006	3015	3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT					
---	---	---	---	---	---
3033	3042	3051	3060	3069	3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT					
---	---	---	---	---	---
3087	3096	3105	3114	3123	3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA					
---	---	---	---	---	---

AAA A 3'

Figure 3: Protein Sequence for I01P3A11.

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILISTS
SMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRTKIGVAADV
RGAALMAPLPVFIKQLPFCSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVL
GLTREAQAKAFGTCVSHVCAVFIFYVPFGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRI
LRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

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Query: 34  GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIIVLIRTSPQLHTPMYLFL 93
          GN + T FIL+GL          L          +Y + ++GNL II ++RT  LH PMY+FL
Sbjct: 6   GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94  SHLAFLDIGYSSSVTPIMLRGFLRKGTFFPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
          L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY
Sbjct: 66  CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP 213
          VAIC PL ++T ++          + + + G          L FC N ++H +C +
Sbjct: 126 VAICHPLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIIVTVFIIALSIVYILVSILKMRSTEGRQKAFSTCTS 273
          ++KL+C          V I S I + +I+ SY+ IL ++L + + E + KAF TC S
Sbjct: 186 VMKLACDDIRNVVYGLIIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTTFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
          H+ AV +F+ + FI + +S ++ +++ Y' +V P+LNP++Y + KE+++
Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQ 302

Query: 330 AMKKL 334
          + +L
Sbjct: 303 RILRL 307

```

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

```

PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
        F+LIG+PGLEEA FW  FPL S+Y +A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
RA1C: 11  FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
        +STS+MPK+LA+FWF+S  I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
RA1C: 71  ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
        HA VL          +IG+ A+VRG+  PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
        NVVYGL  I+  +G+D + IS SY LI++ VL L ++  +AKAFGTCVSH+  V  F
RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTEIRQRILRLFHVA 311
        YVP IGLS+VHRF  D  + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
RA1C: 251 YVPLIGLSVVHREFGNSLDPIVHVLMGDVYLLLPVINPIIYGAKTKQIRTRVLAMFKIS 309

```


Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

```

PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
        F+LIG+PGLE+A FW+ FPL S+Y+++A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
GPCR: 11  FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERS LHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
        +STS+MPK+LA+FWF+S  I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
GPCR: 71  ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLCADD 193
        HA VL      +IG+ AVVRG+      PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRNVVYGLLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
        NVVYGL  I+  +G+D + IS SY LI++TVL L ++  +AKAFGTCVSH+  V  F
GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHREFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTEIRQRILRLFHVA 311
        YVP IGLS+VHREF      + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
GPCR: 251 YVPLIGLSVVHREFGNSLHPIVRVVMGDIYLLLPVINPIIYGAKTKQIRTRVLAMFKIS 309

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Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

```

PHOR: 7  NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
      N +   +F+L G+PGLE +  WL+ PLC +Y +A+ GN  I+  VR E SLHEPMY FL
HOR5: 5  NVTHPAFFLLTGIPGLESSHWSLGSGLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64

PHOR: 67  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
      MLS D+ IS +++P +L F N+  I FDACL+Q+F IH  S MES +LLAM+FDYRV
HOR5: 65  MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
      AIC PLR+ATVLT  +  +G+ A R    + PLP IK+LP CRSN+LSHSYCLH D+
HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPPLFIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
      M+LAC DI +N +YGL V++S G+D  I SY+LIL++V+  +RE + KA TCVSH
HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFIGLSMVHFRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQRIL 305
      + AV  FYVP IG+S VHRF K      + V+++N+YL VPPVLNP++Y  KTKAIR+ I
HOR5: 245 ILAVLAFYVPMIGVSTVHFRFGKHVPCYIHVLMNSVYLFVPPVLNPLIYSAKTKAIRRAIF 304

PHOR: 306 RLFH 309
      R+FH
HOR5: 305 RMFH 308

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